OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: August 19, 2003, 15:20:10 : Search time 290 Seconds
                                               (without alignments)
                                               2271.934 Million cell updates/sec

Title: US-09-494-297-2
Perfect score: 3945
Sequence: 1 MKKTRFPNKLNTLNTQRVLS..........IAGISLGIWGIHTIRIRKHID 757

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 5580241 seqs, 87035780 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                   Maximum Match 100%
                   Listing first 45 summaries

Database :   Pending_Patents_AA_Main:*

                   1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
                   2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
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                  24: /cgn2_6/ptodata/1/paa/US099A_COMB.pep:*
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                  29: /cgn2_6/ptodata/1/paa/US103_COMB.pep:*
                  30: /cgn2_6/ptodata/1/paa/US104_COMB.pep:*
                  31: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Length	DB	ID	Description
1	3945	100.0	757	18	US-09-494-297-2	Sequence 2, Appli
2	1958.5	49.6	742	18	US-09-494-297-4	Sequence 4, Appli

3	223	5.7	770	28	US-10-282-122A-74295	Sequence 74295, A
4	205	5.2	1154	15	US-09-134-000-6122	Sequence 6122, Ap
5	205	5.2	1154	15	US-09-134-000C-6122	Sequence 6122, Ap
6	205	5.2	1154	30	US-10-417-884-4518	Sequence 4518, Ap
7	181	4.6	728	30	US-10-282-122A-52796	Sequence 52796, A
8	180	4.6	597	20	US-09-600-720-18	Sequence 18, Appli
9	180	4.6	597	28	US-10-206-576-404	Sequence 404, App
10	178	4.5	898	11	US-09-445-096A-11	Sequence 11, Appl
11	177	4.5	907	28	US-10-282-122A-62968	Sequence 62968, A
12	176	4.5	905	18	US-09-445-096A-70	Sequence 70, Appl
13	168	4.3	1233	15	US-09-134-000-4971	Sequence 4971, Ap
14	168	4.3	1233	15	US-09-134-000C-4971	Sequence 4971, Ap
15	168	4.3	1233	30	US-10-282-122A-52796	Sequence 52796, A
16	164.5	4.2	833	18	US-10-206-576-404	Sequence 404, App
17	161	4.1	1416	28	US-10-206-576-402	Sequence 402, App
18	161	4.1	1448	28	US-10-282-122A-76871	Sequence 76871, A
19	157.5	4.0	5005	28	US-09-817-514A-2	Sequence 2, Appl
20	157	4.0	888	28	US-10-282-122A-57155	Sequence 57155, A
21	152.5	3.9	1788	28	US-10-282-122A-46664	Sequence 46664, A
22	152.5	3.9	2013	28	US-10-282-122A-60608	Sequence 60608, A
23	152	3.9	1849	28	US-10-242-056-49	Sequence 49, Appl
24	152	3.9	1849	28	US-10-262-794A-49	Sequence 49, Appl
25	152	3.9	2516	23	US-09-817-514A-2	Sequence 2, Appl
26	152	3.9	2516	28	US-10-282-122A-57155	Sequence 57155, A
27	152	3.9	2516	28	US-10-262-794A-47	Sequence 47, Appl
28	149	3.8	1315	28	US-10-242-056-47	Sequence 47, Appl
29	149	3.8	1315	16	US-09-200-650-5	Sequence 5, Appl
30	149	3.8	1315	16	US-09-200-650C-5	Sequence 5, Appl
31	149	3.8	1315	16	US-09-200-650D-5	Sequence 5, Appl
32	149	3.8	1315	31	US-60-066-815-5	Sequence 5, Appl
33	149	3.8	2032	28	US-10-206-576-458	Sequence 458, App
34	149	3.8	2032	28	US-10-206-576-462	Sequence 462, App
35	149	3.8	2032	28	US-10-206-576-466	Sequence 466, App
36	149	3.8	2054	15	US-09-134-000-6612	Sequence 6612, Ap
37	149	3.8	2054	15	US-09-134-000C-6612	Sequence 6612, Ap
38	149	3.8	2054	30	US-10-434-665-6612	Sequence 6612, Ap
39	148.5	3.8	1906	30	US-10-437-963-106000	Sequence 106000,
40	148	3.8	1183	22	US-09-751-708A-45	Sequence 45, Appl
41	148	3.8	1183	22	US-09-791-537-94532	Sequence 94532, A
42	148	3.8	1183	23	US-09-870-759-45	Sequence 45, Appl
43	148	3.8	2159	28	US-10-282-122A-73651	Sequence 73651, A
44	147	3.7	1349	1	PCT-US02-03987-5898	Sequence 5898, Ap
45	147	3.7	1349	1	PCT-US02-03987-13137	Sequence 13137, A

ALIGNMENTS

RESULT 1
US-09-494-297-2
Sequence 2, Application US/09494297
GENERAL INFORMATION:
APPLICANT: PODBIELSKI, ANDREAS
TITLE OF INVENTION: COLLAGEN-BINDING PROTEINS FROM STREPTOCOCCUS PYOGENES
FILE REFERENCE: P0662BUSO/BAS
CURRENT APPLICATION NUMBER: US/09/494,297
CURRENT FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2
LENGTH: 757
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-09-494-297-2

Query Match   100.0%;   Score 3945;   DB 18;   Length 757;
Best Local Similarity   100.0%;
Matches 757;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 MKKTRFPNKLNTLNTQRVLSKNSKRFTVTLVGVFLMIFALVTSMVGAKTVFGLVESSTPN 60
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Db   1 MKKTRFPNKLNTLNTQRVLSKNSKRFTVTLVGVFLMIFALVTSMVGAKTVFGLVESSTPN 60

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Qy   61 AINPDSSSEYRWYGYESYVRGHPYYKQFRVAHDLRVNLEGSRSYQVYCFNLKKAFPLGSD 120
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Db   61 AINPDSSSEYRWYGYESYVRGHPYYKQFRVAHDLRVNLEGSRSYQVYCFNLKKAFPLGSD 120

Qy  121 SSVKKWYKHDGISTKFEDYAMSPRITGTDELNQKLRAVMYNGHPQNANGIMEGLEPLNAI 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 SSVKKWYKHDGISTKFEDYAMSPRITGTDELNQKLRAVMYNGHPQNANGIMEGLEPLNAI 180

Qy  181 RVTQEAVWYYSDNAPISNPDESFKRESESNLVSTSQLSLMRQALKQLIDPNLATKMPKQV 240
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Db  181 RVTQEAVWYYSDNAPISNPDESFKRESESNLVSTSQLSLMRQALKQLIDPNLATKMPKQV 240

Qy  241 PDDFQLSIFESSEDKGDKYNKGYQNLLSGGLVPTKPPTPGDPPMPNQPQTTSVLIRKYAI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PDDFQLSIFESSEDKGDKYNKGYQNLLSGGLVPTKPPTPGDPPMPNQPQTTSVLIRKYAI 300

Qy  301 GDYSKLLEGATLQLTGDNVNSFQARVFSSNDIGERIELSDGTYTLTELNSPAGYSIAEPI 360
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Db  301 GDYSKLLEGATLQLTGDNVNSFQARVFSSNDIGERIELSDGTYTLTELNSPAGYSIAEPI 360

Qy  361 TFKVEAGKVYTIIDGKQIENPNKEIVEPYSVEAYNDFEEFSVLTQNYAKFYAKNKNGS 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 TFKVEAGKVYTIIDGKQIENPNKEIVEPYSVEAYNDFEEFSVLTQNYAKFYAKNKNGS 420

Qy  421 SQVVYCFNADLKSPPDSEDGGKTMTPDFTTGEVKYTHIAGRDLFKYTVKPRDTDPDTFLK 480
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Db  421 SQVVYCFNADLKSPPDSEDGGKTMTPDFTTGEVKYTHIAGRDLFKYTVKPRDTDPDTFLK 480

Qy  481 HIKKVIEKGYREKGQAIEYSGLTETQLRAATQLAIYYFTDSAELDKDKLKDYHGFGDMND 540
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Db  481 HIKKVIEKGYREKGQAIEYSGLTETQLRAATQLAIYYFTDSAELDKDKLKDYHGFGDMND 540

Qy  541 STLAVAKILVEYAQDSNPPQLTDLDFFIPNNNKYQSLIGTQWHPEDLVDIIRMEDKKEVI 600
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Db  541 STLAVAKILVEYAQDSNPPQLTDLDFFIPNNNKYQSLIGTQWHPEDLVDIIRMEDKKEVI 600

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Db  601 PVTHNLTLRKTVTGLAGDRTRKDFHFEIELKNNKQELLSQTVKTDKTNLEFKDGKATINLK 660

Qy  661 HGESLTLQGLPEGYSYLVKETDSEGYKVKVNSQEVANATVSKTGITSDETLAFENNKEPV 720
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Db  661 HGESLTLQGLPEGYSYLVKETDSEGYKVKVNSQEVANATVSKTGITSDETLAFENNKEPV 720

Qy  721 VPTGVDQKINGYLALIVIAGISLGIWGIHITRIRKHD 757
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Db  721 VPTGVDQKINGYLALIVIAGISLGIWGIHITRIRKHD 757
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RESULT 2
US-09-494-297-4
; Sequence 4, Application US/09494297
; GENERAL INFORMATION:
; APPLICANT: PODBIELSKI, ANDREAS
; TITLE OF INVENTION: COLLAGEN-BINDING PROTEINS FROM STREPTOCOCCUS PYOGENES
; FILE REFERENCE: P0662USO/BAS
; CURRENT APPLICATION NUMBER: US/09/494,297
; CURRENT FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-494-297-4

Query Match 49.6%; Score 1958.5; DB 18; Length 742;
Best Local Similarity 54.3%; Pred. No. 2e-156;
Matches 400; Conservative 116; Mismatches 196; Indels 25; Gaps 13;

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Qy   20 SKNSKR--FTVTLVGVFLMIFALVTSMVGAKTVFGLVESSTPNAINPDSSSEYRWGYES 77
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Db   11 SANNKRRQTTIGLLKVFLTFVALIGIVGFSIRAFGAEEQSVPN--RQSSIQDYPWGYDS 68
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Qy   78 YVRGHPYYKQFRVAHDLRVNLEGSRSYQVYCFNLKKAFPLGSDSSVKKWYKHDGISTKF 137
        | .:|| :|| ||||  :| ||||||| |.|||||  ||  ||||    |:|| | |
Db   69 YPKGYPDYSPLKTYHNLKVNLEGSKDYQAYCFNLTKHFPSKSDSVRSQWYKLEGTNENF 128

Qy  138 EDYAMSPRITGTDELNQKLRAVMYNGHPQNANGIMEGLEPLNAI 197
        : .|||||| :||: ::|||   || :  |:| ::|| |||||:
Db  129 IKLADKPRIEDGQLQQNLRILYNGYPNNRNGTMKGIDPLNAILVTQNAIW-YTDSAQI- 186

Qy  198 NPDESFKRESESNLVSTSQLSLMRQALKQLIDPNLATKMPKQVPDDFQLSIFESSEDGDK 257
        |||||||  . ::  | .:| |||:||| |||||| .|   | ||||||||||||:: |
Db  187 NPDESFKTEARSNGINDQQLGLMRKALKELIDPNLGSKYSNKTPSGYRLNVFESHD--- 242

Qy  258 YNKGYQNLLSGGLVPTKPPTPGDPPMPNQPQTTSVLIRKYAIGDYSKLLEGATLQLTGD 317
        :.:||:|||| . ||   | :|   |||    ||| |||| .:|||||||||||:| .
Db  243 --KPFQNLLSAEYVPDTPPKPGEE--PPAKTEKTSVIIRKYAEGD-SKLLEGATLKLSQI 297

Qy  318 NVNSFQARVFSSNDIGERIELSDGTYTLTELNSPAGYSIAEPITFKVEAGKVYTI-IDGK 376
        ::.||| :.||:|| ||:.||| |||||| .||.|||.|||||  :|| .| ||: :|||
Db  298 EGSGFQEKDFQSNSLGEVELNGTYLTETSSPDGYKIAEPITKFRVENKKYFIVQKDGS 357

Qy  377 QIENPNKEIVEPYSVEAYNDFEEFSVLT-TQNYAKFYYAKNKNGSSQVVYCFNADLKSPP 435
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Db  358 QVENPNKEVAEPYSVEAYNDFMDEEVLSGFTPVGKFYYATNKDKSSQVVYCFNADLHSPP 417

Qy  436 DSEDGGKTMTPDFTT--GEVKYTHIAGRDLFKYTVKPRDTDPDTFLKHIKHIKKVIEKGYREKG 494
        || |.| :.||| ::  .|||||| || ||||| ::|||| |:|||:| |||||||||||:::|
Db  418 DSYDSGETINPDSTMKEVKYTHTAGSDLFKYALRPRDTNPEDFLKIHIKKVIEKGYKKKG 477

Qy  495 QAIEYSGLTETQLRAATQLAIYYFTDSAELDKDKL----KDYHGFGDMNDSTLAVAKILV 550
        ::  :.|||||| |||||||||||||||:||  |      | |||| ::|::|||.|  :
Db  478 DS--YNGLTETQFRAATQLAIYYFTDSADLKTLKTYNNGKGYHGFESMDEKTLAVTKELI 535

Qy  551 EYAQDSNPPQLTDLDFFIPNNNKYQSLIGTQWHPEDLVDIIRMEDKK-EVIPVTHNLTLR 609
        .|||:.. |||.:|||::|||.| |||||| .||:||||:|||||||| |||||||:||:
Db  536 TYAQNGSAPQLINLDFFVPNNSKDQSLIGTECHPDDLVDVIRMEDKKKQEVIPVTHSLTVK 595

Qy  610 KTVTGLAGDRTKDFHFEIELKNNKQELLSQTVKTDKTNLEFKDGKATINLKHGESLTLQG 669
        |||  : ||.|| |.||:||| :   ::. |:||:  :|: .|||  ||| |||:| ::|
Db  596 KTVVDEEGDKTKGFQFELELKDKTGQPIVNTLKTNNQDLVAKDGKYSPNLKHGDTIRIEG 655

Qy  670 LPEGYSYLVKETDSEGYKVKVNSQEVANATVSKTGITSDETLAFENNKEPVVPTGVDQKI 729
        || |||| :||   .||.| |::| || :.. | . |:|:   :.|: ::  |||: .
Db  656 LPTGYSYTLKEAEAKDYIVTVDNKVSQEAQSVGKDIIEDKKYTFENRDLVPPTGLITTDG 715

Qy  730 NGYLALIVIAGISLGIW 746
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Db  716 AIYLWLLLLVPLGLLVW 732
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RESULT 3
US-10-282-122A-74295
; Sequence 74295, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23 ; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26 ; PRIOR APPLICATION NUMBER: 60/230,727
; PRIOR FILING DATE: 2000-09-06 ; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06 ; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09 ; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16 ; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2001-02-09 ; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-10-23 ; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-11-27 ; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2000-12-22 ;
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 74295
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-282-122A-74295

Query Match   5.7% ;
Best Local Similarity   21.0% ;   Score 223;   DB 28;   Length 770;
Conservative 108; Pred. No. 8.6e-09;   Length 770;
Matches 158;   Conservative 108;   Mismatches 261;   Indels 226;   Gaps 39;

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Qy   21 KNSKR-FTVLVGVFLMIFALVTSMVGAKTVFGLVESSTPNAINPDSSSEYR------W  72
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Db    4 KNSYKLSFLLSLTG---FILGLLVEFIGLSGV-SVGHAETRNGCANKQGAFEIKNKSQEE  59

Qy   73 YGVESVVRGHPYYKQFRVAHDLRVNLEGSR----SYQVVCFNLKRAFPLGSDSSSVKKW 126
            : :           :  :  ::    :::    ::::::::::::::::::::::::
Db   60 YNYE------VYDNNNILQDGEHKLEIKRVDGTGKTYQGFCFQLTKNFPTRAQGVS-KKL 111

Qy  127 YKKHDGISTKFED------YAMSPR-ITGDELNQKLRAVMYNGHPQNANGIMEGLEPL  177
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Db  112 YKK---LSSSDEETLKQYASKYTSNRGDTSGNLKKQIAKVLTEGYPTNKSDWLNGITEN 168

Qy  178 NAIRVTQEAVWYYSDNAPISNPDESFKRESESNLVSTSQLSLMRQALKQLIDPNLAITKMP 237
          :  ::::: ::   :  :::::::::::::::::::::::::::::::::::::::
Db  169 EKIEVTQDAIWYFTETTVPA---DRSYTNRNVNS------QKMKEVYQKLID---TIDID 216

Qy  238 KQVPDDFQLSIFESEDKGDKYNKGYQNLLSGGLVPTKPPTPGDPPMEPNQPQTTSVLIRK 297
         : :  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db  217 KV--EDVQFDLFVPQD-----TNLQAVIS--VEPVIESLPWTSLKPIAQKDITAKKIWV 266

Qy  298 YAIGD----YSKLLEGATLQLTGDNVNSFQARVFSSNDIGERIELSDGTYTLTELNSPAG 353
          :::     ::::::::::::::::::::::::::::::::::::::::::::::::::
Db  267 DAPKEKPIIYFKLYR----QLPGEK------EVAVDDAELKQINSEGQ 304

Qy  354 YSIAEPITFKV---EAGKVYTIIDGKQIENPNKEIVEPYSVEAYNDF-EEFSVLTQNYA 409
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Db  305 QEISVTWTNQLVTDEKGMAY-IYSVKEVDK-NGELLEP------KDYIKKEDGLTVVN-- 354

Qy  410 KFYYAKNKNGSSQVVVCF-NADLKSPPDSEDGGKTMTPDFTTGEVKYTHIAGRDLFKYTV 468
         : : :::::::::::::  :::::::::::::::::::::::::::::::::::::::::
Db  355 -TYVKPTSGHYDIEVTFGNGHDIDTEDT----TPDIVSGENQMKQIEGED-----S 400

Qy  469 KPRDTDDTFLKHIKKVIEKGYREKGQAIEYSGLTETQLRAATQLAIYYFTDSAELDKDK 528
         :   :::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db  401 KPIDE---------VTENN 410

Qy  529 LKDYHGFGDMNDSTLAVAKILVEYAQDSNPQLTLDDFFIPNNNKYQSLIGTQWHPEDLV 588
         : :  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db  411 ------------LIEFGKNTMPGEEDG----TNSNKYE 432

Qy  589 DIIRMEDKKEVIPVTHNLTLRKTVTGLAGDRTKDFHFEIELKNNKQELLSQTVKTDKTNL 648
         :  :::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db  433 --EVEDSRPV-----DTLSGLSSEQCQSGDMTIEEDSATHIKFSKRDIDGKELAGATMEL 485

Qy  649 EFKDGKATIN--LKHGESLTLQGLPEGYSLVKEFDSEGYKV------KVNSQEVANATV 700
         : ::::      :::::::::::::::::::::::::::::       ::::::::::::
Db  486 RDSSGK-TISTWISDGQVRDFYLMPGKYTF-VEFAAPDGYEVAFAITFTVNEQ--GQVTV 541

Qy  701 SKTGTTSDEFLAFENNKEPVVPTG----VDQKI 729
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Db  542 NGKATKGDAHIVMVDAYKPTKGSGQVIDIEEKL 574
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RESULT 4
US-09-134-000-6122
Sequence 6122, Application US/09134000A
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-005
CURRENT APPLICATION NUMBER: US/09/134,000A
CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 6810
SEQ ID NO 6122
LENGTH: 1154
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000-6122

Query Match   5.2% ;
Best Local Similarity   23.4% ;   Score 205;   DB 15;   Length 1154;
Conservative 85;   Pred. No. 5.9e-07;   Length 1154;
Matches 167;   Conservative 85;   Mismatches 231;   Indels 230;   Gaps 43;

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Qy   96 VNLEGS--RSYQVVCFNLKRAFPLGSDSSSVKKWVKKHDGISTKFED------YAMSPRIT 147
            : :    :::::::::::::::::::::::::::::::::::::      ::::::::
Db  602 VSLIGATINSNEIY--------LGKGQEIQIHIQVR--IQTESENFKPDFWIQMNGRTT 650

Qy  148 GDELNQKLRAVMYNGHPQNANGIMEGLEPLNAIRVTQEAVWYYSDNAPISNPDESFKRES 207
         ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db  651 FQPLATAPEKVDF--------GVPSGKAP--GVKLNVKKIWEEYDQDPFSRPDNVIYEIS 700

Qy  208 ESNLVSTS-----QLSLMRQALKQLIDPNLAITKMPKQVPDDFQ--LSIFESEDKGDKY 258
          :  :::      :::::::::::::::::::::::::::::::   :::::::::::::
Db  701 RKQVTDTANWQTGYIKLSKPENDTSNSWERKNVTQLSKFADESYQEVLGLPQYNNQGQAF 760

Qy  259 NKGYQNLLSGGLVPTKPPTPGDPPMPPNQPQTTSV---LIRKYAIGDYSKLLEGATLQLT 315
          :::::::::::::::::::::::::::::::::::   ::::::::::::::::::::::
Db  761 N--YQTTRELA-VPGYSQEKIDDTTWKNIKQFKPLDLKVIKNSSSGE--KNLVGAVFELS 815

Qy  316 GDNVNSFQARVFSSND----IGERIELSDG-TYTLTELNSPAGYSIAEPITFKVEA---G 367
         ::::::::::::::::    :::::::::: :::::::::::::::::::::::::    :
Db  816 GKNV---QTTLVDNKDGSYSLPKDVRLQKGERYTLTEVKRAPAGHELGKKTTWQIEVSEQG 872

Qy  368 KVYTIIDGKQIENPNKEIVEPYSVEAYNDFEEFSV----LTTQ-----NYAKFYYA---K 415
         ::::::::::::::::::::::::::::::::::::    ::::     ::::: ::   :
Db  873 KV--SIDGQVTTTNQVI--PLEIE--NKRSSLPTRIRKYTMQNGKQVNLAEATFALQRK 926

Qy  416 NKNGSSQVVVCFNADLKSPPDSEDGGKTMTPDFTTGEVKYTHIAGRDLFKYTVKPRDTDP 475
         :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db  927 NAQGSYQTVATQKID------------------------------------TTG------ 944

Qy  476 DTFLKHIKKVIEKG-YREKGQAIEYSGLTETQLRAATQLAIYYFTDSAELDKDKLKDYHG 534
         :::::::::::::  ::::::::::::::::::::::::::::::::::::::::::::::
Db  945 ---LSYF-KISEPGEYR----MVEQSG-----PLGYDTLAGNYEFF--VDK-------- 980

Qy  535 FGDMNDSTLAVAKILVEYAQ--DSNPPQLTLDDFFIPNNNKYQSLIGTQWHPEDLVDII 591
         :::::::::::::::::::   :::::::::::::::::::::::::::::::::::::
Db  981 YGK-------IHYAGKNIEENAPEWT-------------------------------- 999

Qy  592 RMEDKKEVIPVTHNLTLRK--TVTGLAGDRTKDFHFEIELKNNKQELLSQTVKTDKTNL 648
         :::::::::::::::::::   ::::::::::::::::::::::::::::::::::::::
Db 1000 -------------LTHQNNLKPFDLTVHKKADNQT-----------PLKGAKFRLIG--- 1037

Qy  649 EF-KDGKAT------INLKHGE-SLTLQGLPEGYSLVKEFD----SEGYKVKVNSQEVANA 698
         :  ::::::      ::::::  :::::::::::::::::::    :::::::::::::::
Db     -  ---------- 1154
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Db  1038 ELPKDGKETDTFVFENLKPGKYVLTETFTPEGYQGLKEPIELIIREDGSVTIDGEKVADV 1097
             |:| ||  | |:     ||| ||    | ||| ||  | :  || |  :||  |
Qy   699 TVS---KTGITSDETLAFENNKEPVVPTGVDQKINGYLALI---VIAGISLGI 745
          ||| |                        :|  | :|||  ||| |
Db  1098 LISGEKNNQITLDVT---NQAKVPLPETGGIGRLWFYLIAISTFVIAGVYLFI 1147
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RESULT 5
US-09-134-000C-6122
; Sequence 6122, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6122
; LENGTH: 1154
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6122

  Query Match   5.2%; Score 205; DB 15; Length 1154;
  Best Local Similarity   23.4%; Pred. No. 5.9e-07;
  Matches 167; Conservative 85; Mismatches 231; Indels 230; Gaps 43;

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Qy    96 VNLEGS--RSYQVYCFNLKKAFPLGSDSSVKKWYKKHDGISTKFED------YAMSPRIT 147
          |||:|      ::  |  ||: |
Db   602 VSLTGATINSNEIY------------LGKGQEIQIHYQVR--IQTESENFKPDFWYQMNGRTT 650

Qy   148 GDELNQKLRAVMYNGHPQNANGIMEGLEPLNAIRVTQEAVWYYSDNAPISNPDESFKRES 207
          ||
Db   651 FQPLATAPEKVDF------GVPSGKAP--GVKLNVKKIWEEYDQDPTSRPDNVIYEIS 700

Qy   208 ESNLVSTS------QLSLMRQALKQLIDPNLATKMPKQVPDDFQ--LSIFESEDKGDKY 258
             :|         |:
Db   701 RKQVTDTANWQTGYIKLSKPENDTSNSWERKNVTQLSKTADESTQEVLGLPQYNNQGQAF 760

Qy   259 NKGYQNLLSGGLVPTKPPTPGDPMPPNQPQTTSV--LIRKYAIGDYSKLLEGATLQLT 315
          |:                            :||    ||
Db   761 N--YQTTRELA-VPGYSQEKIDDTTWKNTKQFKPLDLKVIKNSSSGE--KNLVGAVFELS 815

Qy   316 GDNVNSFQARVFSSND---IGERIELSDG-TYTLTELNSPAGYSIAEPITFKVEA---G 367
          ||||:|:||||:|||       |:|||| ||:||||||       ::|  || |   |
Db   816 GKNV---QTTLVDNKRDGSYSLPKDVRLQKGERYLTEVKAPAGHELGKKTTWQIEVSEQG 872

Qy   368 KVYTIIDGKQIENPNKEIVEPYSVEAYNDFEEFSV------LTTQ-----NYAKFYYA---K 415
          ||:||||                            |     |||      |||||||   |
Db   873 KV--SIDGQEVTTNQVI--PLEIE--NKFSSLPIRIRKYTMQNGKQVNLAEATFALQRK 926

Qy   416 NKNGSSQVVYCFNADLKSPPDSEDGGKTMTPDFTTGEVKYTHIAGRDLFKYTVKPRDTDP 475
          |
Db   927 NAQGSYQTVATQKTD------TTG 944

Qy   476 DTFLKHIKKVIEKG-YREKGQAIEYSGLTETQLRAATQLAIYYFTDSAELDKDKLKDYHG 534
          ||:|||||| |:|   |||||||||||:||||||||||||||||||||||||||||||||
Db   945 ---LSYF-KISEPGEYR-----MVEQSG-----PLGYDTLAGNYEFT---VDK 980

Qy   535 FGDMNDSTLAVAKILVEYAQ---DSNPPQLTDLDFFIPNNNKYQSLIGTQWHPEDLVDII 591
          |:|
Db   981 YGK------IHYAGKNIEENAPEWT 999

Qy   592 RMEDKKEVIPVTHNLTLRK----TVTGLAGDRTKDFHFEIELKNNKQELLSQTVKTDKTNL 648
          ||                    ||| |||||||||||||||||||||||||||||:|
Db  1000 ------------LTHQNNLKPFDLTVHKKADNQT------PDTDI 1037

Qy   649 EF-KDGKAT-----INLKHGE-SILTLQGLPEGIYSYLVKETD---SEGYKVKVNSQEVANA 698
          |   |||||     | |:|| |  :| | ||||||:  : :|      | | |||:|||:
Db  1038 ELPKDGKETDTFVFENLKPGKYVLTETFTPEGYQGLKEPIELIIREDGSVTIDGEKVADV 1097

Qy   699 TVS---KTGITSDETLAFENNKEPVVPTGVDQKINGYLALI---VIAGISLGI 745
          ||| |                        :|  | :|||  ||| |
Db  1098 LISGEKNNQITLDVT---NQAKVPLPETGGIGRLWFYLIAISTFVIAGVYLFI 1147
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Db  1038 ELPKDGKETDTFVFENLKPGKYVLTETFTPEGYQGLKEPIELIIREDGSVTIDGEKVADV 1097
             |:| ||  | |:     ||| ||    | ||| ||  | :  || |  :||  |
Qy   699 TVS---KTGITSDETLAFENNKEPVVPTGVDQKINGYLALI---VIAGISLGI 745
          ||| |                        :|  | :|||  ||| |
Db  1098 LISGEKNNQITLDVT---NQAKVPLPETGGIGRLWFYLIAISTFVIAGVYLFI 1147
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RESULT 6
US-10-434-665-6122
; Sequence 6122, Application US/10434665
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-09
; CURRENT APPLICATION NUMBER: US/10/434,665
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US 09/134,000
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6122
; LENGTH: 1154
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-434-665-6122

  Query Match   5.2%; Score 205; DB 30; Length 1154;
  Best Local Similarity   23.4%; Pred. No. 5.9e-07;
  Matches 167; Conservative 85; Mismatches 231; Indels 230; Gaps 43;

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Qy    96 VNLEGS--RSYQVYCFNLKKAFPLGSDSSVKKWYKKHDGISTKFED------YAMSPRIT 147
          |||:|      ::  |  ||: |
Db   602 VSLTGATINSNEIY------------LGKGQEIQIHYQVR--IQTESENFKPDFWYQMNGRTT 650

Qy   148 GDELNQKLRAVMYNGHPQNANGIMEGLEPLNAIRVTQEAVWYYSDNAPISNPDESFKRES 207
          ||
Db   651 FQPLATAPEKVDF------GVPSGKAP--GVKLNVKKIWEEYDQDPTSRPDNVIYEIS 700

Qy   208 ESNLVSTS------QLSLMRQALKQLIDPNLATKMPKQVPDDFQ--LSIFESEDKGDKY 258
             :|         |:
Db   701 RKQVTDTANWQTGYIKLSKPENDTSNSWERKNVTQLSKTADESTQEVLGLPQYNNQGQAF 760

Qy   259 NKGYQNLLSGGLVPTKPPTPGDPMPPNQPQTTSV--LIRKYAIGDYSKLLEGATLQLT 315
          |:                            :||    ||
Db   761 N--YQTTRELA-VPGYSQEKIDDTTWKNTKQFKPLDLKVIKNSSSGE--KNLVGAVFELS 815

Qy   316 GDNVNSFQARVFSSND---IGERIELSDG-TYTLTELNSPAGYSIAEPITFKVEA---G 367
          ||||:|:||||:|||       |:|||| ||:||||||       ::|  || |   |
Db   816 GKNV---QTTLVDNKRDGSYSLPKDVRLQKGERYLTEVKAPAGHELGKKTTWQIEVSEQG 872

Qy   368 KVYTIIDGKQIENPNKEIVEPYSVEAYNDFEEFSV------LTTQ-----NYAKFYYA---K 415
          ||:||||                            |     |||      |||||||   |
Db   873 KV--SIDGQEVTTNQVI--PLEIE--NKFSSLPIRIRKYTMQNGKQVNLAEATFALQRK 926

Qy   416 NKNGSSQVVYCFNADLKSPPDSEDGGKTMTPDFTTGEVKYTHIAGRDLFKYTVKPRDTDP 475
          |
Db   927 NAQGSYQTVATQKTD------TTG 944

Qy   476 DTFLKHIKKVIEKG-YREKGQAIEYSGLTETQLRAATQLAIYYFTDSAELDKDKLKDYHG 534
          ||:|||||| |:|   |||||||||||:||||||||||||||||||||||||||||||||
Db   945 ---LSYF-KISEPGEYR-----MVEQSG-----PLGYDTLAGNYEFT---VDK 980

Qy   535 FGDMNDSTLAVAKILVEYAQ---DSNPPQLTDLDFFIPNNNKYQSLIGTQWHPEDLVDII 591
          |:|
Db   981 YGK------IHYAGKNIEENAPEWT 999

Qy   592 RMEDKKEVIPVTHNLTLRK----TVTGLAGDRTKDFHFEIELKNNKQELLSQTVKTDKTNL 648
          ||                    ||| |||||||||||||||||||||||||||||:|
Db  1000 ------------LTHQNNLKPFDLTVHKKADNQT------PDTDI 1037
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```
Qy   649  EF-KDGKAT------INLKHGE-SLTLQGLPEGYSYLVKETD---SEGYKVKVNSQEVANA 698
          ||||            ||: |: ||||||||||:|||| |    :|||:|:||||:||
Db  1038  ELPKDGKETDTFVFENLKPGKVYLTETFTPEGYQGLKEPIELIIREDGSVTIDGEKVADV 1097

Qy   699  TVS--KTGITSDETLAFENNKEPVVPTGVDQKINGYLALI---VIAGISLGI 745
          |||   |:|||||  |||| ||| |  | ||| ||||     | |||||| |
Db  1098  LISGEKNNQITLDVT---NQAKVPLPETGGIGRLWFYLIAISTFVIAGVYLFI 1147
```

RESULT 7
US-10-417-884-4518
Sequence 4518, Application US/10417884

GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm   and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
    ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/417,884
FILING DATE: 17-Apr-2003

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 4518:
SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium

FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1..728

SEQUENCE DESCRIPTION: SEQ ID NO: 4518:
US-10-417-884-4518

Query Match 4.6%; Score 181; DB 30; Length 728;
Best Local Similarity 20.7%; Pred. No. 2.9e-05;
Matches 147; Conservative 102; Mismatches 235; Indels 226; Gaps 37;

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Qy   96  VNLEGS--RSYQVYCFNLKKAPPLGSDSSVKKWYKHDGISTKFEDY--------- 141
         :::||    :|:|||| | |      ||  |  | |  |::|||:
Db  175  ISIEGNIKSNQIY--------LGKDQEIQIHYQVR--IQTENEDFHPNFWYQMNGRTT 223

Qy  142  MSPRITGDELNQKLRAVMYNGHPQNANGIMEGLEPLNAIRVTQEAVWYYSDNAPISNPDE 201
Db  224  FQPNIDTNELAE--------------FGIPSAKAPGVSLHI--KKLWEEFDNNLADRPDQ 267
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RESULT 8
US-09-600-720-18
Sequence 18, Application US/09600720

GENERAL INFORMATION:
APPLICANT: GUSS, Bengt et al.
TITLE OF INVENTION: NOVEL FIBRONECTIN-BINDING PROTEIN
FILE REFERENCE: 0825-0161P
CURRENT APPLICATION NUMBER: US/09/600,720
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0

SEQ ID NO 18
LENGTH: 597
TYPE: PRT
ORGANISM: Streptococcus equi
US-09-600-720-18

Query Match 4.6%; Score 180; DB 20; Length 597;
Best Local Similarity 20.8%; Pred. No. 2.5e-05;
Matches 149; Conservative 102; Mismatches 265; Indels 202; Gaps 34;

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Qy  202  -SFKRESESNLVSTSQGLSLMRQALKQLIDPNLAT---------KMPKQVPDDFQ--LSI 248
         ||||||||||||||||||||||||||||||       |      | ||:|:| |  |::
Db  268  VTFEIORE----HTTNAAAWKNGYIRIIKPAKDTNTWERADIDKLSAHSGESYQEILSL 323

Qy  249  FESEDKGDKYNKGYQNLLSGGLVPTKPPTPG-----DPPMPPNQPQTTSV--LIRKYA 299
         ||||||  ||||          ||| |   |     ||    |:| |  |   | |||
Db  324  POYNNQQOAFS--YQTI------KELPVPGYDSQQIDAMTWKNTKQFTPLNLKITKNSS 374

Qy  300  IGDYSKLLEGATLQLTGDNVNSFQA-RVFSSNDIGERIEL--SDGTYTLTELNSPAGYSIA 357
         ||| ||   ||| ||||| :  :     | :||||| | |  ||||| | |   | ||::
Db  375  TGE--KDLIGAVFKLTGDSIDTLLTDHGDGTYSLPENVKLQOKEMYTLLETKAPGGHGLS 432

Qy  358  EPIIFKVEAGKVYII-IDGK------------QIENPNKEIVEPISVEANYNDFEEFSVLTT 405
         ||    ||||:|||| ||||            |||||:|| ||  :|||
Db  433  KKTTWEIKIASDGTVTIIDGKTVTTSDDTIQLTIENPFVEV--PVAVRKYAQMQGTDKEINL 490

Qy  406  QNYAKFYYAKNKNGSSQVVYCFNADLKSPPDSE---DGGKTMTPDFTTGEVKYTHIAGRD 462
         |: | |  ||:|||| |||| | ||   |:|:    |||  :||| |||| ||: ||
Db  491  KGAAFSLQKKEANGTYQ-------PIDSQTTNEKGLASFDSLTPGKYRVVETAGPA 539

Qy  463  LFKYTVKPRDTDPDTFLKIHKKVIEKGYRREKGQAIEYSGLTETQLRAATQLAIYYFTDSA 522
         |  |   | |   :   | || :: |||:      |:  ||   ||:       | |
Db  540  GY-------DTSPGNYEFQIDKY------------GKII-YTGKNTEMTNNVWLTHQNRLKAF 583

Qy  523  ELDKDKLKDYHGFGDMNDSTLAVAKILVEYAQODSNPPQLTDLDFFIPNNNKYQSLIGTQW 582
          |   |  |    |  ||  |  ||:|   | |      |   ||:||||:||:||
Db  584  DLTVHKKED------NGQOTLKGAFRIQ-----GPEM-DLE------ 612

Qy  583  HPEDLVDIIRMEDKKEVIPVTHNLTLRKTVTGLAGDRTKDFHFEELKNNKQELLSQTVK 642
                                                     |:|:|  ||||:| |
Db  613  SPKD------GQETDFLEE------ 626

Qy  643  TDKTNLEFFKDGKAATINLKHGE-SLTLQGLPEGYSYLI---VKETDSEGYKVKVNSQEVANA 698
                         |:|||||  ||||||||||||||    :|||||:||||||||:||
Db  627  ----------NLKPGTYTLTETFTPEGYQGLKEPVTIVIHEDGSIOVDGQD--HE 669

Qy  699  TVSKTGITSDE-TLAFENN-KEPVVPTGVDQKINGYLALIVIAGISLGIW 746
         :|| |||:|||  ||| ||  |:|||||||||||||| :|:| |  |:||
Db  670  SVLSPGAKNNQISLDITNQAKVPLPETGGIGRLGIY--LVGMIGCAFSIW 717
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RESULT 9
US-10-269-017-18
; Sequence 18, Application US/10269017
; GENERAL INFORMATION:
; APPLICANT: GUSS, Bengt et al.
; TITLE OF INVENTION: NOVEL FIBRONECTIN-BINDING PROTEIN
; FILE REFERENCE: 0825-0127P
; CURRENT APPLICATION NUMBER: US/10/269,017
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 18
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Streptococcus equi
US-10-269-017-18

Query Match   20.8%; Score 180; DB 28; Length 597;
Best Local Similarity   102; Pred No. 2.5e-05;
Matches 149; Conservative 102; Mismatches 265; Indels 202; Gaps 34;

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Qy  233 ATKMPKQVPDDFQLSIFESEDKGDRYNKGYQNLLSGGLVPTKPPTPGDPMPMPNQPQTTS 292
Db  201 DSKL-KSEQSNYSLDIVYQSGGGHDHMKDYQNLLGSTLIPKEPLKP------------- 245

Qy  293 VLIRKYAIGDYSKLLEGATLQLTGDNVNSFQARVFSSNDIGERIELSDGTYTLTELNSPA 352
Db  246 ------QLGGFS-----GHNGNGLSGLEGGSSGSQOETNE--DGKKGL--IGFHG 284

Qy  353 GYSIAE-----PIT-FKVEAGKVYTIIDGKQIENPNKEIVEPYSVEAYNDFEEFSVLTTQ 407
Db  285 GLSGSEGKRDPLPGLKGEAGAPDT------PQKPNDPL---QGLEGGN-----SPIVEQN 330

Qy  408 YAKFYYAKNKNGSSQVVYCFNADLKSPPDSEDGGKTMTPDFTTGEVKYTHIAG------R 461
Db  331 YGS---TEGYHQOSGILE--ETEDTNPPGIILGGSGNVE--THEDTRNPHLMGIGGGLAG 383

Qy  462 DLFKYTVKPR--------DTDPDTFLKHIKKVIEKGYREKGQAIEYSGLITEQLRAATQ 512
Db  384 ESGETTPKPGQTGQGQPVIETTEDT---------QKGMSGQSGGTIESENTKKPE 429

Qy  513 LAIYYFTDSAELDKDKLKDYHGFGDMNDSTLAVAKILVEYAQDSNPQLTDLDFFIPNNN 572
Db  430 VMIGGQGQTIETTEDTQK-----GMSGQSGGTIE------SEDTKKPEV-------- 467

Qy  573 KYQSLIGTQWHPEDLVDIIRMEDKKEVIPVTHNLFLRKTVTGLAGDRTKDFHFEIELKNN 632
Db  468 ----MIGGQ------GQIIDFSEN--TOSGMSGQSGDTT------VIEDTK 500

Qy  633 KQELLSQTVKTDKTNLEFKDGKATINLKHGESLTLQGL--PEGYSYLVKETDSEGYKVKV 690
Db  501 KSEII---IGGQGQIIDFSED------TQPGMSGQSGGTTIVEDIKKPPTPKKP 545

Qy  691 NSQEVANATVSKTGITSDETLAFENNKEPVVPTGVDQK-----INGYLALIVIAGISL 743
Db  546 APAPIVN--------DE---KPNKGTHLPQTSDMKQLTLSIIGAMSMLLVLCLSL 589
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Query Match   4.6%; Score 180;
Best Local Similarity   102; Mismatches 149; Conservative 102;
Matches 149;

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Qy   68 SEYRWYGYESYVR-GHPYYKQFRVAHDLRVNLEGSRSYQVYCFNLKKAFPLGSDSSVKKW 126
Db   32 AEQLYYGWNDGTROSSPYF--LYVSPKNAPKRELKDEYVYCFNKLYWPDQWESIYSNF 89

Qy  127 -----YKKHDGISTKFEDYAMSPRITGDELNQKLRAVMYNGHPQONANGIMEG- 173
Db   90 NDIRSPYNDLPVYEKKLGTDGIFKQYAPDYKKDISDIASRAIVAVLSNGYPTNKSQLSTSY 149

Qy  174 -LEPLNAIRYTQEAVWYYSDNAPISNPDESFKRESESNLVSTSQLSLMRQALKQLIDPNL 232
Db  150 HLNNDSSRKYTQLALTWYFSD----SLTKEYLKDTGGYNL----NDMEKKALDFLISKGE 200

Qy  233 ATKMPKQVPDDFQLSIFESEDKGDRYNKGYQNLLSGGLVPFKPPTPGDPMPMPNQPQTTS 292
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RESULT 10
US-09-445-096A-11
; Sequence 11, Application US/09445096A
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Du, Run-Pan
; APPLICANT: Wang, Quijun
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; FILE REFERENCE: 1038-989 MIS
; CURRENT APPLICATION NUMBER: US/09/445,096A
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 08/867,941
; PRIOR FILING DATE: 1997-06-03
; PRIOR APPLICATION NUMBER: PCT/CA98/00544
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-445-096A-11

Query Match   4.5%; Score 178; DB 18; Length 898;
Best Local Similarity   18.6%; Pred No. 7.6e-05;
Matches 171; Conservative 118; Mismatches 305; Indels 324; Gaps 42;

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Db  201 DSKL-KSEQSNYSLDIVYQSGGGHDHMKDYQNLLGSTLIPKEPLKP------------- 245
Qy  293 VLIRKYAIGDYSKLLEGATLQLTGDNVNSFQARVFSSNDIGERIELSDGTYTLTELNSPA 352

Db  246 ------QLGGFS-----GHNGNGLSGLEGGSSGSQOETNE--DGKKGL--IGFHG 284
Qy  353 GYSIAE-----PIT-FKVEAGKVYTIIDGKQIENPNKEIVEPYSVEAYNDFEEFSVLTTQ 407

Db  285 GLSGSEGKRDPLPGLKGEAGAPDT------PQKPNDPL---QGLEGGN-----SPIVEQN 330
Qy  408 YAKFYYAKNKNGSSQVVYCFNADLKSPPDSEDGGKTMTPDFTTGEVKYTHIAG------R 461

Db  331 YGS---TEGYHQOSGILE--ETEDTNPPGIILGGSGNVE--THEDTRNPHLMGIGGGLAG 383
Qy  462 DLFKYTVKPR--------DTDPDTFLKHIKKVIEKGYREKGQAIEYSGLITEQLRAATQ 512

Db  384 ESGETTPKPGQTGQGQPVIETTEDT---------QKGMSGQSGGTIESENTKKPE 429
Qy  513 LAIYYFTDSAELDKDKLKDYHGFGDMNDSTLAVAKILVEYAQDSNPQLTDLDFFIPNNN 572

Db  430 VMIGGQGQTIETTEDTQK-----GMSGQSGGTIE------SEDTKKPEV------- 467
Qy  573 KYQSLIGTQWHPEDLVDIIRMEDKKEVIPVTHNLFLRKTVTGLAGDRTKDFHFEIELKNN 632

Db  468 ----MIGGQ------GQIIDFSEN--TOSGMSGQSGDTT------VIEDTK 500
Qy  633 KQELLSQTVKTDKTNLEFKDGKATINLKHGESLTLQGL--PEGYSYLVKETDSEGYKVKV 690

Db  501 KSEII---IGGQGQIIDFSED------TQPGMSGQSGGTTIVEDIKKPPTPKKP 545
Qy  691 NSQEVANATVSKTGITSDETLAFENNKEPVVPTGVDQK-----INGYLALIVIAGISL 743

Db  546 APAPIVN--------DE---KPNKGTHLPQTSDMKQLTLSIIGAMSMLLVLCLSL 589
```

Query Match   4.5%; Score 178; DB 18; Length 898;
Best Local Similarity   18.6%; Pred No. 7.6e-05;
Matches 171; Conservative 118; Mismatches 305; Indels 324; Gaps 42;

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Qy    4 TRFPNKLNTLNTQRVLSKNSRFTVTLVGVFLMIFALVTSMVGAKIVFGLIVESSTPNAIN 63
Db   79 TTDPNGDNNQLTQ------AQKTAAAAGFVM---------- 115

Qy   64 PDSSSE--YRWYG--YESYVRGHP------------YYKQFRVAHDLRVNL 98
Db  116 PDYSNDLVQQWQGKLIVGIDAHRPDGIGTGKNLRQPTTANDIKPLIYFNKFPALSDLHLDS 175

Qy   99 EGSRSYQVYCFNLKKAFPLGSDSSVKK--WKKHDGISTKFEDYAMSP-------RIT 147
```

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

RESULT 11
US-10-282-122A-62968
Sequence 62968, Application US/10282122A
GENERAL INFORMATION:

Query Match 4.5%; Score 177; DB 28; Length 907;
Best Local Similarity 20.6%; Pred. No: 9.4e-05;
Matches 164; Conservative 104; Mismatches 262; Indels 268; Gaps 40;

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Qy   84 YYKQFRVAHDLRVNLEGSRSYQVYCFNLKKA----FPLGSDSSVKK--WYKKHDGI 133
Db  165 YFDKFPKISDL--HLENSE---HVFDAKKANNIKIYGYCALSSPAKNPTYMNYQQENI 218
Qy  134 STK--FEDYA----MSPRIT----GDELNQKLRAVMYNG----HPQNANGIMEGL 174
Db  219 KNKKPGDDYQNIRFGYMELRELDLNKKGADTQSDKNRAIIFTTPTLFYHGENASTHLP-- 276
Qy  175 EPLNAIRVTQEAVWYYSDNAP----ISNPDE-----SFKRESESNLVSTSQLSL---- 219
Db  277 --KAGKPFDYEGNWLYLTDVKRRPFLDKVGTYFNSTRKSNEGDLVSAAHIYLNSFK 333
Qy  220 ------MRQALKQLIDPNLATKMPKQVPDDF------QLSIFESEDK-- 254
Db  334 YKHTPATYSVFDQNTLKGRLSYYDNPNKQTADGRYIRSQFDTDKKVNEADVYEIDAKIN 393
Qy  255 GDKYNKGYQNLLSGGL------VPTKPPFPGDPMPPNQPQTTSVLIRKYAIGDYSKL 306
Db  394 GNRFGTGTAKSLIIDDNTNTAPFVKELFSKKANPNNP--DPN------SDT 434
Qy  307 LEGATLQLTGDNVNSFQARVFSSNDI------GERIELSDGTYLTLELNSPAGYSIAEP 359
Db  435 LEGGFYGESGDEL----AGKFLSNDNATFVVFGGKRDKITTEPVATKTVYFS-TGFE--KP 487
Qy  360 ITFKVEAGKVYTIIDGK---QIENPNKEIVEPYSVEAYNDF------EEFSVLTT 405
Db  488 STSFVGNEEIGSIIDGKKLNDEVNNQIEDETVPVSNKEYEYNYGRPNKQFTKKINASVQ 547
Qy  406 QNYA-----KFYY----AK--NKNGSSQVVYCFNADLKSPPDSEDGGKTMTPDFT 449
Db  548 KNPAYFGQHDKFYFYFNGNYYDLSAKEANKLGVSQDTSTNKSILARKYPDA---KVSTDNKV 603
Qy  450 T------GEVKYTHIAGRDLFKYTVKPRDTDPDTFLK---- 480
Db  604 TKIVLQQAKDKPYTAIHAKSYDHISFGEVLYNDNKGNPTRSYFVQGGADVSTQLPSAGK 663
Qy  481 ------HIKKVIEKGYREKGQAIEYSGLTETQLRAATQLAIYYFT------DSAEL 524
```

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Db  176 ERHR-FDPKKLNTIKVYGYGNLTTPSKNNTIYINHQQADNKKNNKPVDPYENIRFGYLELQ 234
Qy  148 GDELNQK------LRAVMYNGHPQNANGIMEGLEPLN------ 178
Db  235 GSSLTQKNADTPNDKDRIPKPMPILFYHG--ENASSQLPSAGKFNYTGNWLYLSDVKKRP 292
Qy  179 AIRVTQEAVWYSDNAPISNPEDESFKRESESNLVSTSQLSL------ 219
Db  293 ALSASDDRVGYVLNASGKSN------EGDVVSAAHIYLNGFQYKHTPATYQVDPDTN 343
Qy  220 -MRQALKQLIDPNLATKMPKQVPDDF------QLSIFESEDK--GDKYNKGYQNLLSGG 269
Db  344 SLTGKLSYYDNPNQQTAQGKYIKSQFDTTKKVNETDVYQIDAKINGNRFVGTAKSLVNEN 403
Qy  270 L------VPTKPPFPGDPMPPNQPQTTSVLIRKYAIGDYSKILLEGATLQLTGDNVNS 321
Db  404 TETAPFIKELFSKKANPNNP--NPN------SDTLEGGFYGESGDEL-- 442
Qy  322 FQARVFSSND------IGERIELSDGTYTLTFELNSPAGYSIAEPITFKVEAGKVYTIIDG 375
Db  443 -AGKFLSNDNASYVVFGGKRDKTDKPVATKTVYFSAGFE--KPSTSFVDNETIGRIINS 498
Qy  376 KQIENPNKEIVE-----PYSVEAYNDF-----EEFSVLTTQN----YAKFYYAK 415
Db  499 KKLNDAVNEKIDNGDIPTSDERYDEFPWGEKKAEFTKKVSSSTQAVPAYFGQHDKFYF-- 556
Qy  416 NKNGSSQVVYCFNADLKSPPDSEDGGKTMTPDFTTGEV------ 453
Db  557 -NGNYDLSASSVDKLAPADAVKANQSIKEKYPNATLNKDNQVTAIVLQEARDNKPYTA 614
Qy  454 ---KYTHIA-GRDLF------KYTVKPRDTDPDTFLKHIKKVI----- 486
Db  615 IRAKSYQHISPGETLYNDANQTPTRSYFVQGGRADTSTTLPKAGKFTYNGLWAGYLIQKK 674
Qy  487 EKGYREKGQAIEYSG-----LITETQLRAATQLAIYYFT------DSAELDKDKLKDYHGF 535
Db  675 DKGYSNNEETIKKKGHGODYLITED------FTPEDDDDLTASDDSQDDDAHGD 722
Qy  536 GDMNDSTLAVAKILVEYAQDSNPPQLTDLDFFIPNNNKYQSLIGTQWHPEDLVDIIRMED 595
Db  723 DDL------IASDSDQDDDADGDDDSDDL--GDGADDAAAGKVYHAGN---IRPEF 767
Qy  596 KKEVIPV--THNLTL-----RKTVTGLAGDRTKDFHFEIELKNKQELL 637
Db  768 ENKYLPINEPTHEKTFPALDGKNKAKPDVDFDTNSLTGKLNDERGDIVFDI--KNGKIDGT 825
Qy  638 SQTVKTDKTNLEFKDGKATINLKHGESLTLQGLPEGYSYLVKETDSEGYKVKVNSQEVA- 696
Db  826 GFTAKADVPNYREEVG---NNQGG------GFLYNIKDIDVKGQFFGTNGEELAG 871
Qy  697 ------NATVSKTG 704
Db  872 QLQYDKGDGINDTAERAG 889
```

```
Db 664  FTYNGLWAGYLTQKKDKGTYSKDEDIIKQKGLKD----------YILTKDFIPQDDDDD 712
Qy 525  DKDKL--------KDYHGFGDMNDSTLAVAKILVEYAQDSNPPQLTDLDFFIPNNKYQS 576
Db 713  DDDSLTASDSDSQDDNTHGDDDL------IASDDSQDDADGDDDSDDL--GDGADDD 761
Qy 577  LIGTQWHPEDLVDIIRMEDKKEVIPV----------THNLTL------RKTVTGLAGD 618
Db 762  AAGKYTHAGN----IRPEFENKYLPINEPTHEKTFALDGKNKAKFDVNFDTNSLTGKLND 817
Qy 619  RTKDFHFEIELKNNKQELLSQTVKTDKTNLEFKDGKATINLKHGESLTLQGLPEGYSYLV 678
Db 818  ERGDIVFDI--KNGKIDGTGFTAKADVPNYREEVG--------GFLYNI 861
Qy 679  KETDSEGYIKVKVNSQEVA 696
Db 862  KDIDVKGQFPGTNGEELA 879
```

RESULT 12
US-09-445-096A-70
Sequence 70, Application US/09445096A
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M.
APPLICANT: Du, Run-Pan
APPLICANT: Wang, Quijun
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
FILE REFERENCE: 1038-989 MIS
CURRENT APPLICATION NUMBER: US-09/445,096A
CURRENT FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 08/867,941
PRIOR FILING DATE: 1997-06-03
PRIOR APPLICATION NUMBER: PCT/CA98/00544
PRIOR FILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 70
LENGTH: 905
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-09-445-096A-70

```
Query Match         4.5%;    Score 176;   DB 18;   Length 905;
Best Local Similarity   20.6%;   Pred. No. 0.00011;
Matches 164;  Conservative 102;  Mismatches 264;  Indels 266;  Gaps 40;

Qy  84  YKQFRVAHDLRVNLEGSRSYQVYCFNLKKA----FPLGSDSSVKK----WYKKHDGI 133
Db 165  YFDKFPKISDL-HLENSE----HVFDAKANNIKIYGYGALSSPAKNPTYMNYQQEQNI 218

Qy 134  STK--FEDYA-----MSPIT-----GDELNQKLRAVMYNG-----HPQNANGIMEGL 174
Db 219  KNKKPGDDYQNIRPGVMELRELDLNKKGADNQSDKNRAIIFTTPLFYHGENASTHLP-- 276

Qy 175  EPLNAIRVTQEAVWYYSDNAP----ISNPDE------SFKRESESNLVSTSOLSI--- 219
Db 277  ---KAGKFDYEGNWLYLTDVKKRPFLDKTDDKVGTYFNSTRKSNEGDLVSAAHIVLNSFK 333

Qy 220  ---------------MRQALKQLIDPNLATKMPKQVPDDF-----QLSIFESEDK-- 254
Db 334  YKHPATYSVDFDQNTLKGKLSYYDNPNKQTADGRYIRSQFDTDKKVNEADVYEIDAKIN 393

Qy 255  GDKYNKGYQNLLSGGL------VPTKPPTPGDPMPPNQPQTTSVLIRKYAIGDYSKL 306
Db 394  GNRETGTAKSLIDDNTNTAPFVKELFSKKANPNNP-DPN----------SDT 434

Qy 307  LEGATLQLTGDNVNSFQARVFSSNDI-----GERIELSDGTYLTELNSPAGYSIAEP 359
Db 435  LEGGFYEGESGDEL----AGKFLSNDNATFVVFGGKRDKITEPVAIKTVYFS-TGFE--KP 487
```

```
Qy 360  ITFKVEAGKVYTIIDGK------QIENPNKEIYEPYSVEAYNDF--------EEFSVLTT 405
Db 488  STSFVGNEEIGSIIDGKGLNDEVNNQIEDETVPVSNKEYYEYNYGRPNKQFTKKINASVQ 547
Qy 406  QNYA------KFYY------AK--NKNGSSQVVYCFNADLKSPEDSEDGGKTMIFDFT 449
Db 548  KNPAYFGQHDKFYFNGNYYDLSAKEANKLGVSQDTSTNKSILAKYPDA----KVSTDNKV 603
Qy 450  T------------------GEVKYTHIAGRDLFKYTVKPRDTDPDTFLK---- 480
Db 604  TKIVLQQAKDKPYTAIHAKSYDHISFGEVLYNDKNGNPTRSYFVQGGQADVSTQLPSAGK 663
Qy 481  -------HIKKVIERGYREKGQAIEYSGLTETQLRAATQLAIYYFT------ 519
Db 664  FTYNGLWAGYLTQKGKGKDGGYSKDEDTIKQKGLKD------------YILTKDFIPQDDDDD 712
Qy 520  DSAELDKDKLKD-YHGFGDMNDSTLAVAKILVEYAQDSNPPQLTDLDFFIPNNKYQSLI 578
Db 713  DSLTASDDSQDDDNTHGDDDL------IASDDSQDDTPDGDDDSDDL--GDGADDDAA 761
Qy 579  GTQWHPEDLVDIIRMEDKKEVIPV-----THNLTL------RKTVTGLAGDRT 620
Db 762  GKVYHAGN----IRPEFENKYLPINEPTHEKTFALDGKNKAKFDVNFDTNSLTGKLNDER 817
Qy 621  KDFHFEIELKNNKQELLSQTVKTDKTNLEFKDGKATINLKHGESLTLQGLPEGYSYLVKE 680
Db 818  GDIVFDI--KNGKIDGTGFTAKADVPNYREEVG--------GFLYNIKD 861
Qy 681  TDSEGYIKVKVNSQEVA 696
Db 862  IDVKGRFFGTNGEELA 877
```

RESULT 13
US-09-134-000-4971
Sequence 4971, Application US/09134000A
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
TITLE OF INVENTION: FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-005
CURRENT APPLICATION NUMBER: US/09/134,000A
CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 6810
SEQ ID NO 4971
LENGTH: 1233
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000-4971

```
Query Match         4.3%;    Score 168;   DB 15;   Length 1233;
Best Local Similarity   21.5%;   Pred. No. 0.00093;
Matches 163;  Conservative 105;  Mismatches 323;  Indels 168;  Gaps 42;

Qy  39  ALVTSMVGAKIVFGLVES---STPNAINPDSSSEYRWYGYESYVRGHPYYKQFRVAHDLR 95
Db 515  SLSTPVIGPNRAIQLVSDQYIEPISVVNP-LNAETAWGNYDQ------NGAYSSR 562

Qy  96  --VNLEGSRSYQVYCFNLKKAFP----LGSDSSVKKWYKIHDGISTKFEDYAMSPRITGD 149
Db 563  TTVSVWGSKERPIQNLEIKVKHPNVLSLRATKEIYFYK----LGT---DYTVTPTSDGS 615

Qy 150  ELNQKLRAVMYNGHPQNANGIMEGLE-----PLNAIRVTQEAVWYYSDNAPISNPDESFK 204
Db 616  VIKFTPPITNEIQIPIGFNVYPDSLPKDKSIPVDTIPITMSAEGLTPVDTIVTT--NSK 672

Qy 205  RESESNLVSTSQLSLMRQALKQLIDPNLATKMPKQVPDDFQLSIFESEDKGDKYNKGYQN 264
Db 673  RGSERTLQSSKNQFLVNARNDSFDSLSVRTKIPAGA--DVLFDIDVSN--DQVDSIYPQ 728

Qy 265  LLSGGLVPTKPPTPGDPMP--PNQPQTTSVLI------RKYAIGDYSKL---LEGATLQ 313
Db 729  YWDRGQYFDKPMTPNSPGYPTITFDBNTNSYTFDFGKTNKRYII-EYKNANGWIDVPTLY 787
```

RESULT 14
US-09-134-000C-4971
Sequence 4971, Application US/09134000C

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 03279G-032
CURRENT APPLICATION NUMBER: US-09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 4971
LENGTH: 1233
TYPE: PRT
ORGANISM: Enterococcus faecalis

US-09-134-000C-4971

Query Match   4.3%;   Score 168;   DB 15;   Length 1233;
Best Local Similarity   21.5%;   Pred. No. 0.00093;
Matches 163;   Conservative 105;   Mismatches 323;   Indels 168;   Gaps 42;

```
Qy   39 ALVTSMVGAKTVFGLVES------STPNAINPDSSSEYRWYGVESYVRGHPYYKQFRVAHDLR 95
Db  515 SLSTPVIGPNKAIQLVSDQYIEPISVVNP-LNAETAWGNYDQ-----------NGAYSSR 562

Qy   96 --VNLEGSRSYQVYCFNLKKAFP------LGSDSSVKWYKKHDGISTKFEDYAMSPRITGD 149
Db  563 TTVSVMGSKEKPIQNLEIKVKHPNYLSLRATKEIYFYK----LGT---DYTVPTPSDGS 615

Qy  150 ELNQKLRAVMYNGHPQNANGIMEGLE-----PLNAIRVTQEAVWYYSDNAPISNPDESEK 204
Db  616 VIKFTTPTINEIQIPIGFNYVPVPDSLPKDKSIPVDTIPITMSAEGLTPVDTITVT---NSK 672

Qy  205 RESESNLVTSTQSLSLMRQALKQLIIDPNLATKMPKQVPDDFQOLSTPESEDKGDKYNKGIQN 264
Db  673 RGSERTIQSSKNQFLVNARNDSFDSLSVRTKIPAGA---DVLFDIYDVSN--DQVDSIYPQ 728

Qy  314 LTG------------DNVNSFQARVFSSNDIGERIELSDGTYTLTELNSPAGYSIAEPITFKVEAG 367
Db  788 ITGTAKEPQSNNNEGSASVSVQN--EALDILSAT---------------QAANPLKNVTKT 832

Qy  368 KVYT-IIDGK--QIENPNKEIVEPYSVEAXNDFEEFSVLTQNYAKFYAKNKNGSSQVV 424
Db  833 TVTTKNIDNKTHRVKNPTIELTPKGTTNAQIDLNSITV----------KGVPEDA 877

Qy  425 YCFNADLKSPPDSEDGGKTMTPDFTTGE---VKYTHIAGRDLFKYTVKPRDTPDTFLKH 481
Db  878 Y-----------SLEKTTNGAKVIFKDYTLTENTIIEYNTVSANAGQIYTETTIDSETLNQMSA 930

Qy  482 IKKVI-------------EKGYREKGQAIEYSGLTETQLRAATQLAIYYFTD---SAEL 524
Db  931 SKKKVTTAPITLKFSEGDAEGIVYLATATFYTHNVEDENQAIAKVSFELIDNVTHTATEF 990

Qy  525 DKDKLKDYHGFGDM-NDSTLAVAKILVEYAQDSNPPQLT--------DLDFFIP---- 569
Db  991 TTDEKGQYSFDAIMTGDYTLRVTNVPQEYSVDEE--YLTGKAIKLVKGDNQLKIPLTKTI 1048

Qy  570 NNNKYQ------SLIGTQWHPEDLVDIIRMEDKK-EVIPVTHNLFLRKTVTGLAGDRTKDF 623
Db 1049 DHSRLQVKDSTIYVGDSWKPEE---NFVSATDKTGQDVPFE------KITVSGQV-DNTKAG 1100

Qy  624 HFEIELKN-NKQELLSQTVKTDKTNLEFKDGKATINLKHGESLTLQGLPEGYSYLVKETD 682
Db 1101 VYPIIYSDEGKEETAYVTVKPDQSKLEVKD--TTIYV--GDSWK----PE--DNFVSATD 1150

Qy  683 SEGYKV---KVNSQEVANATVSKTGITSDETLAFENNKE 718
Db 1151 KTGQDVPFEKIDVQGTVN--VDKIG---DYEIVYKNGKK 1184
```

RESULT 15
US-10-434-665-4971
Sequence 4971, Application US/10434665

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH03-09
CURRENT APPLICATION NUMBER: US/10/434,665
CURRENT FILING DATE: 2003-05-14
PRIOR APPLICATION NUMBER: US 09/134,000
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 4971
LENGTH: 1233
TYPE: PRT
ORGANISM: Enterococcus faecalis

US-10-434-665-4971

Query Match   4.3%;   Score 168;   DB 30;   Length 1233;
Best Local Similarity   21.5%;   Pred. No. 0.00093;
Matches 163;   Conservative 105;   Mismatches 323;   Indels 168;   Gaps 42;

```
Qy   39 ALVTSMVGAKTVFGLVES------STPNAINPDSSSEYRWYGVESYVRGHPYYKQFRVAHDLR 95
Db  515 SLSTPVIGPNKAIQLVSDQYIEPISVVNP-LNAETAWGNYDQ-----------NGAYSSR 562

Qy   96 --VNLEGSRSYQVYCFNLKKAFP------LGSDSSVKWYKKHDGISTKFEDYAMSPRITGD 149
Db  563 TTVSVMGSKEKPIQNLEIKVHPNYLSLRATKEIYFYK----LGT---DYTVPTPSDGS 615

Qy  150 ELNQKLRAVMYNGHPQNANGIMEGLE-----PLNAIRVTQEAVWYYSDNAPISNPDESFK 204

Qy  265 LLSGGLVPTKPPTPGDPPMP--PNQPQTTSVLI------RKYAIGDYSKL---LEGATLQ 313
Db  729 YWDRGQYFDKPKFMTPNSPGYPIITFDENTNSYTFDFGKTNKRYII-EYKNANGWIDVPTLY 787

Qy  314 LTG------------DNVNSFQARVFSSNDIGERIELSDGTYTLTELNSPAGYSIAEPITFKVEAG 367
Db  788 ITGTAKEPQSNNNEGSASVSVQN--EALDILSAT---------------QAANPLKNVTKT 832

Qy  368 KVYT-IIDGK--QIENPNKEIVEPYSVEAXNDFEEFSVLTQNYAKFYAKNKNGSSQVV 424
Db  833 TVTTKNIDNKTHRVKNPTIELTPKGTTNAQIDLNSITV----------KGVPEDA 877

Qy  425 YCFNADLKSPPDSEDGGKTMTPDFTTGE---VKYTHIAGRDLFKYTVKPRDTPDTFLKH 481
Db  878 Y-----------SLEKTTNGAKVIFKDYTLTENIIEYNTVSANAGQIYTETTIDSETLNQMSA 930

Qy  482 IKKVI-------------EKGYREKGQAIEYSGLTETQLRAATQLAIYYFTD---SAEL 524
Db  931 SKKKVTTAPITLKFSEGDAEGIVYLATATFYTHNVEDENQAIAKVSFELIDNVTHTATEF 990

Qy  525 DKDKLKDYHGFGDM-NDSTLAVAKILVEYAQDSNPPQLT--------DLDFFIP---- 569
Db  991 TTDEKGQYSFDAIMTGDYTLRVTNVPQEYSVDEE--YLTGKAIKLVKGDNQLKIPLTKTI 1048

Qy  570 NNNKYQ------SLIGTQWHPEDLVDIIRMEDKK-EVIPVTHNLTLRKTVTGLAGDRTKDF 623
Db 1049 DHSRLQVKDSTIYVGDSWKPEE---NFVSATDKTGQDVPFE------KITVSGQV-DNTKAG 1100

Qy  624 HFEIELKN-NKQELLSQTVKTDKTNLEFKDGKATINLKHGESLTLQGLPEGYSYLVKETD 682
Db 1101 VYPIIYSDEGKEETAYVTVKPDQSKLEVKD--TTIYV--GDSWK----PE--DNFVSATD 1150

Qy  683 SEGYKV---KVNSQEVANATVSKTGITSDETLAFENNKE 718
Db 1151 KTGQDVPFEKIDVQGTVN--VDKIG---DYEIVYKNGKK 1184
```

```
Db   616  VIKFTPITNELQIPIGFNYVPDSLPKDKSIPVDTIPITMSAEGLTPVDTTVTT---NSK  672
               |  :|:  |   |   |:|  | :  | |  :: |  | |       :|
Qy   205  RESESNLVSTSQLSLMRQALKQLIDPNLATKMPKQVPDDFQLSIFESEDKGDKYNKGYQN  264
          | |:   : |:  |:: |  :    ||:                 : :|     |:
Db   673  RGSERTLQSSKNQFLVNARNDSFDSLSVRTKIPAGA--DVLFDIYDVSN--DQVDSIYPQ  728

Qy   265  LLSGGLVPTKPPTPGDPPMP--PNQPQTTSVLI------RKYAIGDYSKL---LEGAFLQ  313
          | | |: |||:| |      ::| |  : :         | |  |   :: ||
Db   729  YWDRGQYFDKPMTPNSPCYPTTFDENTNSYTFDFGKTNKRYII-EYKNANGWIDVPTLY  787

Qy   314  LTG------DNVNSFQARVFSSNDIGERIELSDGTYLTELNSPAGYSIAEPITFKVEAG  367
          :|:|        :::|         |    |  |    |    |  |  :     ||
Db   788  ITGTAKEPQSNNNEGSASVSVQN---EALDILSAT---------QAANPTLKNVTKT  832

Qy   368  KVYT-IIDGK--QIENPNKEIVEPYSVEAYNDFEEFSVLTQNYAKFYYAKNKNGSSQVV  424
          | |:  | |    :::| ||   |   |   :  |                :| :
Db   833  TVTTKNIDNKTHRVKNPTIELTPKGTTNAQIDLNSITV----------------KGVPEDA  877

Qy   425  YCFNADLKSPPDSEDGGKTMTPDFTTGE---VKYTHIAGRDLFKYTVKPRDTDPPDTFLKH  481
               | |            |||          |  |    |||||     || |  |
Db   878  Y------SLEKTTNGAKVIFKDYTLTENITIEYNTVSANGQIYTETTIDSETLNQMSA  930

Qy   482  IKKVI--------------EKGYREKGQAIEYSGLIETQLRAATQLAIIYYFID----SAEL  524
          |: |:                : :   |   ||: :|  :|     |  :    ||:|
Db   931  SKKKVTTAPITLKFSEGDAEGIVYLATATFYTHNVEDENQAIAKVSFELIDNVTHTATEF  990

Qy   525  DKDKLRKDYHGFGGDM-NDSTLAVAKILVEYAQDSNPPQLT----------DLDFFIP----  569
          | |       |         |  :|  |    | :        |       |  |:|
Db   991  TTDEKGQYSFDAIMTGDYTLRVTNVPQEYSVDEE--YLTGKAIKLVKGDNQLKIPLTKTI  1048

Qy   570  NNNKYQ-----SLIGTQWHPEDLVDIIRMEDKK-EVIPVTHNLTLRKTVTGLIAGDRTKDF  623
          :::|  |      |::  | | | | :  :||    : |:  | | | |: ||  ||  |
Db   1049  DHSRLQVKDSTIYVGDSWKPEE--NFVSATDKTGQDVPFE----KITVSGQV-DNTKAG  1100

Qy   624  HFEIELKN-NKQELLSQTVKTDKTNLEFKDGKATINLKHGESLTLQGLPEGYSYLVKETD  682
          | | :  |  ||:   |:| : | ||||:  ||| ||| ||: ||  | || ||| |
Db   1101  VYPIIYSDEGKEETAVVTVKPDQSKLEVKD--TTIYV--GDSWK-----PE--DNFVSATD  1150

Qy   683  SEGYKV---KVNSQEVANATVSKTGITSDETLAFENNKE  718
          |||:      ||:| ||| | |: | |||: | ||:|:
Db   1151  KTGQDVPFEKIDVQGTVN--VDKIG---DYEIVKNGKK  1184
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